



(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

*66*  
*Concise*

Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln
1				5					10					15	
Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	Tyr
			20					25					30		
Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln
		35					40					45			
Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	50					55					60				
Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg
65					70					75					80
His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro
				85					90					95	
Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
			100					105							

---



SEQUENCE LISTING

B6  
T510Y  
(1) GENERAL INFORMATION:

(i) APPLICANT: CROWE, JAMES SCOTT  
LEWIS, ALAN PETER

(ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
- (B) STREET: 555 THIRTEENTH ST. N.W.
- (C) CITY: WASHINGTON
- (D) STATE: D. C.
- (E) COUNTRY: U.S.
- (F) ZIP: 20004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/952640
- (B) FILING DATE: 01-DEC-1992
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: ERNST, BARBARA G
- (B) REGISTRATION NUMBER: 30,377
- (C) REFERENCE/DOCKET NUMBER: 1808-118

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (202) 783-6040
- (B) TELEFAX: (202) 783-6031



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACATTCAGC TGACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCAAGCTT CTAACACTCT CCCC

24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AACAGCTATG ACCATG

16

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTTTCCCAG TCACGAC

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGTCAGGGT GCTGCTGAGG

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGGGAAGA TGAAGACAGA

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCAGCAGGC ACACAACAGA

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 35..92

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 93..1465

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 35..1465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG	52
Met Asp Trp Thr Trp Arg	
-19 -15	
TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG	100
Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln	
-10 -5 1	
GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG	148
Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr	
5 10 15	
GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC	196
Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser	
20 25 30 35	
TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC	244
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile	
40 45 50	
ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA	292
Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg	
55 60 65	
GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG	340

B6  
Conte

Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	His	Met	Glu	Leu	
		70					75					80				
ACT	AGC	CTG	AGA	TCT	GAG	GAC	ACG	GCC	GTG	TAT	TAC	TGT	GCG	ACA	GAT	388
Thr	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Asp	
	85					90					95					
CGC	TAC	AGG	CAG	GCA	AAT	TTT	GAC	CGG	GCC	CGG	GTT	GGC	TGG	TTC	GAC	436
Arg	Tyr	Arg	Gln	Ala	Asn	Phe	Asp	Arg	Ala	Arg	Val	Gly	Trp	Phe	Asp	
100					105					110					115	
CCC	TGG	GGC	CAG	GGC	ACC	CTG	GTC	ACC	GTC	TCC	TCA	GCC	TCC	ACC	AAG	484
Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
				120					125					130		
GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	532
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	
			135					140					145			
GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	580
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
	150						155					160				
GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	628
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
	165					170						175				
TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	676
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	
180					185					190					195	
GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	ACC	TAC	ATC	TGC	AAC	724
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	
				200					205					210		
GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	GTT	GAG	CCC	772
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	
			215					220					225			
AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	820
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
	230						235					240				
CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	868
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
	245					250					255					
ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	916
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
260					265					270					275	

B6  
Carter

GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC 964  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 280 285 290

GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC 1012  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 295 300 305

AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG 1060  
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 310 315 320

CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA 1108  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA 1156  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350 355

CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC 1204  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn  
 360 365 370

CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC 1252  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 375 380 385

GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC 1300  
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 390 395 400

ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG 1348  
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 405 410 415

CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC 1396  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 420 425 430 435

TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC 1444  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 440 445 450

TCC CTG TCT CCG GGT AAA TGAGTGCAC GGCCGGCAAG CCCCCGCTCC 1492  
 Ser Leu Ser Pro Gly Lys  
 455

CCGGGCTCTC GCGGTGCGAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG 1552

CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA 1612

AAAAA 1617

B6  
Continue



(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly  
-19 -15 -10 -5

Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys  
1 5 10

Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe  
15 20 25

Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
30 35 40 45

Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser  
50 55 60

Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
65 70 75

Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val  
80 85 90

Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala  
95 100 105

Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val  
110 115 120 125

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
130 135 140

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
145 150 155

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
160 165 170

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
175 180 185

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
190 195 200 205

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 210 215 220  
 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 225 230 235  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 240 245 250  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 255 260 265  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 270 275 280 285  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 290 295 300  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 305 310 315  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 320 325 330  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 335 340 345  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 350 355 360 365  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 370 375 380  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 385 390 395  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 400 405 410  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 415 420 425  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 430 435 440 445  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 450 455

B6  
 Contar

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 32..739

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 89..739

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 32..86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC 52  
Met Ala Trp Ala Leu Leu Leu  
-19 -15

CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG 100  
Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ser Ala Leu  
-10 -5 1

ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC 148  
Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile  
5 10 15 20

TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC 196  
Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ser Tyr Asn Leu Val Ser  
25 30 35

TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG 244  
Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ile Met Ile Tyr Glu  
40 45 50

GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG 292  
Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys  
55 60 65

TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC 340

Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp  
 70 75 80

GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT 388  
 Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val  
 85 90 95 100

TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC 436  
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala  
 105 110 115

CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC 484  
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn  
 120 125 130

AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG 532  
 Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val  
 135 140 145

ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG 580  
 Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu  
 150 155 160

ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC 628  
 Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser  
 165 170 175 180

TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC 676  
 Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser  
 185 190 195

TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT 724  
 Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro  
 200 205 210

ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC 776  
 Thr Glu Cys Ser  
 215

TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG 836

CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAAA 896

AAAAAA 902

B6  
 Continues

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

*BL  
Continue*

Met	Ala	Trp	Ala	Leu	Leu	Leu	Leu	Thr	Leu	Leu	Thr	Gln	Asp	Thr	Gly	
-19				-15					-10						-5	
Ser	Trp	Ala	Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	
			1				5					10				
Pro	Gly	Gln	Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Asn	Asn	Asp	Val	
	15					20					25					
Gly	Ser	Tyr	Asn	Leu	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	
30				35					40						45	
Pro	Lys	Ile	Met	Ile	Tyr	Glu	Val	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	
			50						55					60		
Asn	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	
			65					70					75			
Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Cys	Ser	Tyr	
		80					85					90				
Ala	Gly	Ser	Tyr	Thr	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	
	95					100					105					
Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	
110				115						120					125	
Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	
			130						135					140		
Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	
			145					150					155			
Pro	Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	
		160					165					170				
Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	
	175					180					185					
Lys	Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	
190					195					200					205	
Val	Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser						
				210					215							

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA 48  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT 96  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr  
20 25 30

TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144  
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC 192  
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly  
50 55 60

AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC 288  
Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile  
85 90 95

ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA 321  
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

*B6*  
*Continue*

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Tyr
			20					25						30	
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Thr	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	
Glu	Asp	Ser	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Leu	Ile
				85					90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

B6  
Continue

GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA	48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	
1 5 10 15	
GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT	96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr	
20 25 30	
TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC	144
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile	
35 40 45	
TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC	192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly	
50 55 60	
AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	
GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC	288
Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr	
85 90 95	
AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA	324
Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg	
100 105	



(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

*B6  
Cartier*

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asp	Tyr	
		20					25						30			
Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Glu	Leu	Leu	Ile	
		35				40						45				
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65				70					75					80		
Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Gln	His	Thr	Tyr	Ser	Asp	Pro	Tyr	
			85					90						95		
Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg					
		100						105								

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA .

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA 48  
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT 96  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr  
20 25 30

TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144  
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC 192  
Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240  
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC 288  
Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu  
85 90 95

ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324  
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
100 105

B6  
Contue

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

*B6*  
*Carb*

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Thr	Tyr	
			20					25					30			
Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
Tyr	Tyr	Ala	Asn	Ser	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
	65				70					75					80	
Glu	Asp	Ser	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Asn	Ser	Tyr	Pro	Leu	
				85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105								

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA 48  
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly  
1 5 10 15

GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT 96  
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr  
20 25 30

TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC 144  
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile  
35 40 45

TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC 192  
Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly  
50 55 60

AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC 288  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu  
85 90 95

ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324  
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

*b6  
cyste*

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Gln	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala	Ser	Gln	Ser	Leu	Ser	Asn	Tyr	
		20					25						30			
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ile	Pro	Lys	Leu	Leu	Ile	
	35					40						45				
Tyr	Arg	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50				55					60						
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65				70					75					80		
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Asn	Tyr	Gly	Thr	Pro	Leu	
			85					90						95		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
		100					105									

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCCGTCA GTCTTGGAGA GTCGGCCTCC 60  
ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120  
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC 180  
AGGTTCACTG GCAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT 240  
GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA 300  
GGGACCAAGG TGGAAATCAG ACGA 324

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly  
1 5 10 15  
Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Arg Phe Thr Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala  
65 70 75 80  
Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Arg Ser Pro Trp  
85 90 95  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg  
100 105

56  
C-1

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

6  
Continue

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly
1				5				10						15	
Glu	Ser	Ala	Ser	Ile	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25						30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35				40						45		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Asp	Xaa	Xaa	Thr	Xaa
			50				55					60			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Arg	Val	Glu	Ala
65					70					75					80
Xaa	Xaa	Val	Gly	Val	Xaa	Xaa	Xaa	Met	Xaa	Ala	Leu	Arg	Ser	Pro	Trp
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Val	Xaa	Xaa	Arg	Arg				
			100					105							



(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

66  
entire

GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCT	TCC	CTG	TCT	GCA	TCG	GTA	GGA	48
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAC	AGA	GTC	ACC	ATC	ACC	TGC	AGG	GCA	AGT	CAG	GGC	ATT	AGC	GAT	TAT	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asp	Tyr	
			20					25					30			
TTA	AGT	TGG	TAT	CAG	CAG	AAA	CCA	GGA	AAA	GCT	CCT	AAG	CTC	CTG	ATC	144
Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	GCT	GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGC	GGC	192
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
AGT	GGA	TCT	GGG	ACA	GAA	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAA	CCT	240
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
	65				70					75				80		
GAA	GAT	TTT	GCA	ACT	TAT	TAC	TGT	CTA	CAG	GGT	TAT	GGT	ACC	CCG	TAC	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Tyr	Gly	Thr	Pro	Tyr	
			85					90					95			
AGT	TTT	GGC	CAG	GGG	ACC	AAA	GTG	GAG	ATC	AAA	CGA					324
Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105								

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

*B6  
Continue*

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asp	Tyr	
		20					25						30			
Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35				40						45				
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65				70					75					80		
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly	Tyr	Gly	Thr	Pro	Tyr	
			85					90						95		
Ser	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
		100					105									

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

6  
B  
Contour

GAC	ATT	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTG	GGA	48
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAC	ACA	GTC	ACC	ATC	ACT	TGT	CGG	GCA	AGT	CAG	GAC	ATT	AGC	AAT	AAT	96
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Asn	
			20					25					30			
TTA	GTC	TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	144
Leu	Val	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	GCT	GCA	TCC	AGA	TTG	CAA	GAT	GGG	GTC	CCA	TCA	AGG	TTC	AGC	GGC	192
Tyr	Ala	Ala	Ser	Arg	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
AGT	GGG	TCT	GGG	ACC	GAT	TTC	ACC	CTC	ACA	ATT	AAT	CCT	GTG	GAA	GCT	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Pro	Val	Glu	Ala	
	65				70					75				80		
GAC	GAT	GCT	GCG	GAT	TAC	TAC	TGT	CTA	CAG	ACT	AAG	AGT	TCT	CCT	CGG	288
Asp	Asp	Ala	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Thr	Lys	Ser	Ser	Pro	Arg	
				85					90					95		
ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGA					324
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100						105							

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

*6*  
*Continue*

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Asn	
			20					25					30			
Leu	Val	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
Tyr	Ala	Ala	Ser	Arg	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Pro	Val	Glu	Ala	
65					70					75					80	
Asp	Asp	Ala	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Thr	Lys	Ser	Ser	Pro	Arg	
				85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105								